FIG.1A

```
1
CAT CAT AAT GGA ACA AAT GGT ACT ATG ATG CAA TAT TTC GAA TGG TAT TTG CCA AAT GAC
H   H   N   G   T   N   G   T   M   M   Q   Y   F   E   W   Y   L   P   N   D

21
GGG AAT CAT TGG AAC AGG TTG AGG GAT GAC GCA GCT AAC TTA AAG AGT AAA GGG ATA ACA
G   N   H   W   N   R   L   R   D   D   A   A   N   L   K   S   K   G   I   T

41
GCT GTA TGG ATC CCA CCT GCA TGG AAG GGG ACT TCC CAG AAT GAT GTA GGT TAT GGA GCC
A   V   W   I   P   P   A   W   K   G   T   S   Q   N   D   V   G   Y   G   A

61
TAT GAT TTA TAT GAT CTT GGA GAG TTT AAC CAG AAG GGG ACG GTT CGT ACA AAA TAT GGA
Y   D   L   Y   D   L   G   E   F   N   Q   K   G   T   V   R   T   K   Y   G

81
ACA CGC AAC CAG CTA CAG GCT GCG GTG ACC TCT TTA AAA AAT AAC GGC ATT CAG GTA TAT
T   R   N   Q   L   Q   A   A   V   T   S   L   K   N   N   G   I   Q   V   Y
```

FIG.1B

```
101
GGT GAT GTC GTC ATG AAT CAT AAA GGT GGA GCA GAT GGT ACG GAA ATT GTA AAT GCG GTA
G   D   V   V   M   N   H   K   G   G   A   D   G   T   E   I   V   N   A   V

121
GAA GTG AAT CGG AGC AAC CGA AAC CAG GAA ACC TCA GGA GAG TAT GCA ATA GAA GCG TGG
E   V   N   R   S   N   R   N   Q   E   T   S   G   E   Y   A   I   E   A   W

141
ACA AAG TTT GAT TTT CCT GGA AGA GGA AAT AAC CAT TCC AGC TTT AAG TGG CGC TGG TAT
T   K   F   D   F   P   G   R   G   N   N   H   S   S   F   K   W   R   N   Y

161
CAT TTT GAT GGG ACA GAT TGG GAT CAG TCA CGC CAG CTT CAA AAC AAA ATA TAT AAA TTC
H   F   D   G   T   D   W   D   Q   S   R   Q   L   Q   N   K   I   Y   K   F

181
AGG GGA ACA GGC AAG GCC TGG GAC TGG GAA GTC GAT ACA GAG AAT GGC AAC TAT GAC TAT
R   G   T   G   K   A   W   D   W   E   V   D   T   E   N   G   N   Y   D   Y
```

FIG.IC

```
201
CTT ATG TAT GCA GAC GTG GAT ATG GAT CAC CCA GAA GTA ATA CAT GAA CTT AGA AAC TGG
L   M   Y   A   D   V   D   M   D   H   P   E   V   I   H   E   L   R   N   W

221
GGA GTG TGG TAT ACG AAT ACA CTG AAC CTT GAT GGA TTT AGA ATA GAT GCA GTG AAA CAT
G   V   W   Y   T   N   T   L   N   L   D   G   F   R   I   D   A   V   K   H

241
ATA AAA TAT AGC TTT ACG AGA GAT TGG CTT ACA CAT GTG CGT AAC ACC ACA GGT AAA CCA
I   K   Y   S   F   T   R   D   W   L   T   H   V   R   N   T   T   G   K   P

261
ATG TTT GCA GTG GCT GAG TTT TGG AAA AAT GAC CTT GGT GCA ATT GAA AAC TAT TTG AAT
M   F   A   V   A   E   F   W   K   N   D   L   G   A   I   E   N   Y   L   N

281
AAA ACA AGT TGG AAT CAC TCG GTG TTT GAT GTT CCT CTC CAC TAT AAT TTG TAC AAT GCA
K   T   S   W   N   H   S   V   F   D   V   P   L   H   Y   N   L   Y   N   A
```

FIG.1D

```
301
TCT AAT AGC GGT GGT TAT TAT GAT ATG AGA AAT ATT TTA AAT GGT TCT GTG GTG CAA AAA
S   N   S   G   G   Y   Y   D   M   R   N   I   L   N   G   S   V   V   Q   K

321
CAT CCA ACA CAT GCC GTT ACT TTT GTT GAT AAC CAT GAT TCT CAG CCC GGG GAA GCA TTG
H   P   T   H   A   V   T   F   V   D   N   H   D   S   Q   P   G   E   A   L

341
GAA TCC TTT GTT CAA CAA TGG TTT AAA CCA CTT GCA TAT GCA TTG GTT CTG ACA AGG GAA
E   S   F   V   Q   Q   W   F   K   P   L   A   Y   A   L   V   L   T   R   E

361
CAA GGT TAT CCT TCC GTA TTT TAT GGG GAT TAC TAC GGT ATC CCA ACC CAT GGT GTT CCG
Q   G   Y   P   S   V   F   Y   G   D   Y   Y   G   I   P   T   H   G   V   P

381
GCT ATG AAA TCT AAA ATA GAC CCT CTT CTG CAG GCA CGT CAA ACT TTT GCC TAT GGT ACG
A   M   K   S   K   I   D   P   L   L   Q   A   R   Q   T   F   A   Y   G   T
```

FIG. IE

```
401
CAG CAT GAT TAC TTT GAT CAT CAT GAT ATT ATC GGT TGG ACA AGA GAG GGA AAT AGC TCC
Q   H   D   Y   F   D   H   H   D   I   I   G   W   T   R   E   G   N   S   S

421
CAT CCA AAT TCA GGC CTT GCC ACC ATT ATG TCA GAT GGT CCA GGT GGT AAC AAA TGG ATG
H   P   N   S   G   L   A   T   I   M   S   D   G   P   G   G   N   K   W   M

441
TAT GTG GGG AAA AAT AAA GCG GGA CAA GTT TGG AGA GAT ATT ACC GGA AAT AGG ACA GGC
Y   V   G   K   N   K   A   G   Q   V   W   R   D   I   T   G   N   R   T   G

261
ACC GTC ACA ATT AAT GCA GAC GGA TGG GGT AAT TTC TCT GTT AAT GGA GGG TCC GTT TCG
T   V   T   I   N   A   D   G   W   G   N   F   S   V   N   G   G   S   V   S

481
GTT TGG GTG AAG CAA TAA
V   W   V   K   Q   •
```

FIG. 2A

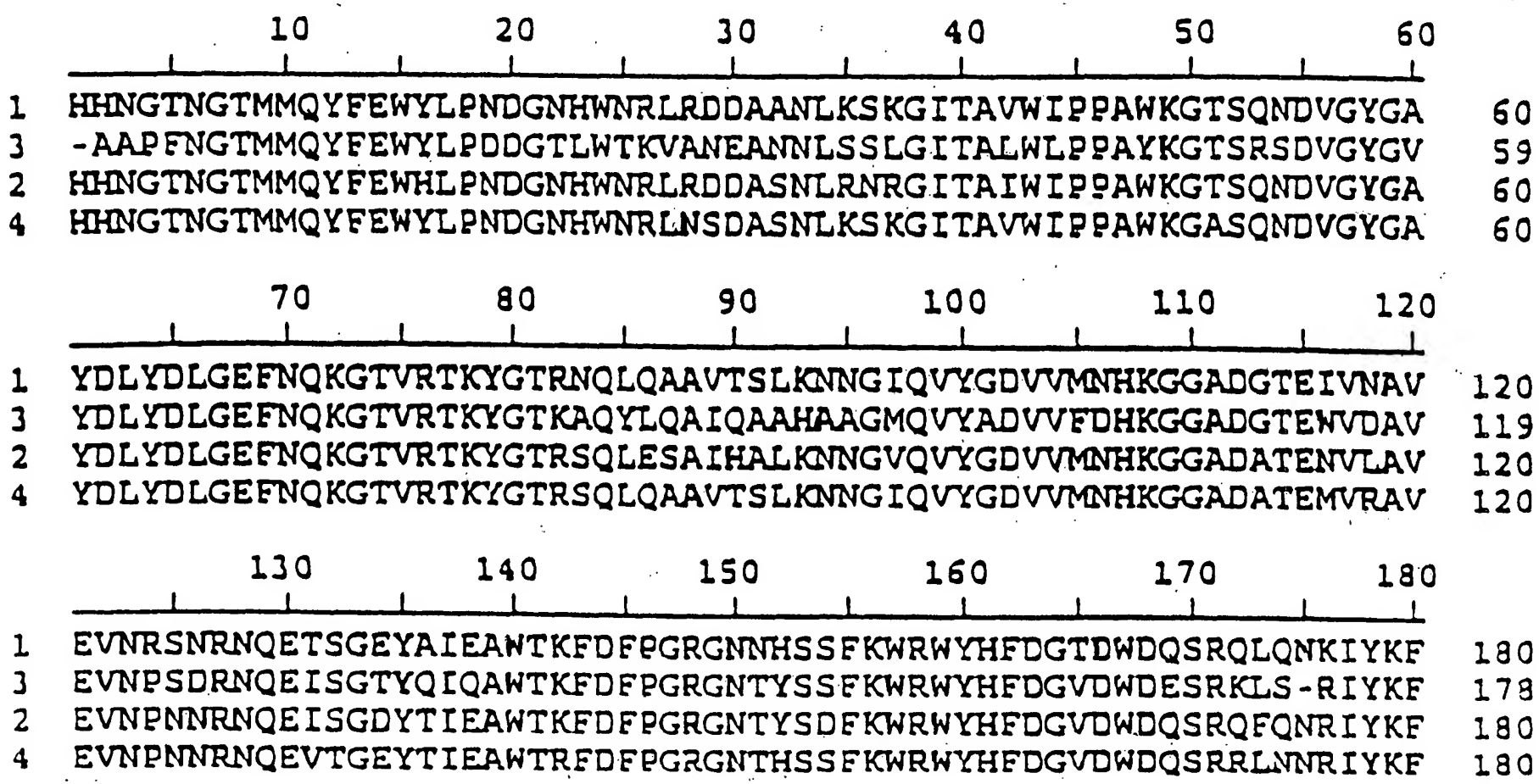
10 20 30 40 50 60
1 HHNGTNGTMMQYFEWYLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA 60
3 -AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGV 59
2 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDASNLRNRGITAIWIPPAWKGTSQNDVGYGA 60
4 HHNGTNGTMMQYFEWYLPNDGNHWNRLNSDASNLKSKGITAVWIPPAWKGASQNDVGYGA 60
70 80 90 100 110 120
1 YDLYDLGEFNQKGTVRTKYGTRNQLQAAVTSLKNNGIQVYGDVVMNHKGGADGTEIVNAV 120
3 YDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAV 119
2 YDLYDLGEFNQKGTVRTKYGTRSQLESAIHALKNNGVQVYGDVVMNHKGGADATENVLAV 120
4 YDLYDLGEFNQKGTVRTKYGTRSQLQAAVTSLKNNGIQVYGDVVMNHKGGADATEMVRAV 120
130 140 150 160 170 180
1 EVNRSNRNQETSGEYAIEAWTKFDFPGRGNNHSSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
3 EVNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLS-RIYKF 178
2 EVNPNNRNQEISGDYTIEAWTKFDFPGRGNTYSDFKWRWYHFDGVDWDQSRQFQNRIYKF 180
4 EVNPNNRNQEVTGEYTIEAWTRFDFPGRGNTHSSFKWRWYHFDGVDWDQSRRLNNRIYKF 180

FIG. 2B

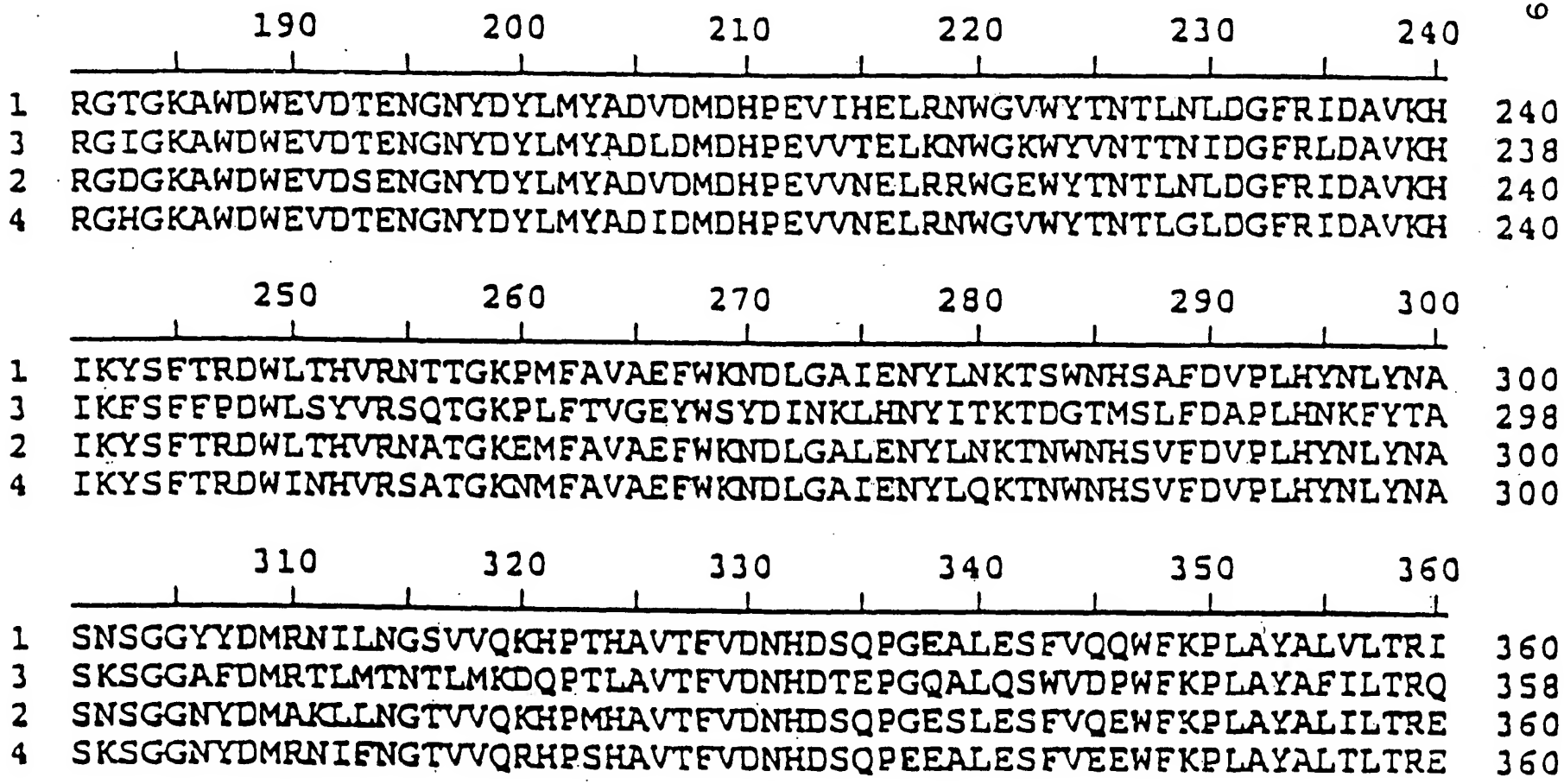
190 200 210 220 230 240
1 RGTGKAWDWEVDTENGNYDYLMYADVDMDHPEVIHELRNWGVWYTNTLNLDGFRIDAVKH 240
3 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKH 238
2 RGDGKAWDWEVDSENGNYDYLMYADVDMDHPEVVNELRRWGEWYTNTLNLDGFRIDAVKH 240
4 RGHGKAWDWEVDTENGNYDYLMYADIDMDHPEVVNELRNWGVWYTNTLGLDGFRIDAVKH 240
250 260 270 280 290 300
1 IKYSFTRDWLTHVRNTTGKPMFAVAEFWKNDLGAIENYLNKTSWNHSAFDVPLHYNLYNA 300
3 IKFSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFYTA 298
2 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHSVFDVPLHYNLYNA 300
4 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLQKTNWNHSVFDVPLHYNLYNA 300
310 320 330 340 350 360
1 SNSGGYYDMRNILNGSVVQKHPTHAVTFVDNHDSQPGEALESFVQQWFKPLAYALVLTRI 360
3 SKSGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQ 358
2 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSQPGESLESFVQEWFKPLAYALILTRE 360
4 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVDNHDSQPEEALESFVEEWFKPLAYALTLTRE 360

FIG. 2C

```
                370        380        390        400        410        420
                |          |          |          |          |          |
1  QGYPSVFYGDYYGIPTHGVPAMKSKIDPLLQARQTFAYGTQHDYFDHHDIIGWTREGNSS   420
3  EGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTE   418
2  QGYPSVFYGDYYGIPTHSVPAMKAKIDPILEARQNFAYGTQHDYFDHHNIIGWTREGNTT   420
4  QGYPSVFYGDYYGIPTHGVPAMRSKIDPILEARQKYAYGKQNDYLDHHNIIGWTREGNTA   420

                430        440        450        460        470        480
                |          |          |          |          |          |
1  HPNSGLATIMSDGPGGNKWMYVGKNKAGQVWRDITGNRTGTVTINADGWGNFSVNGGSVS   480
3  KPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVS   478
2  HPNSGLATIMSDGPGGEKWMYVGQNKAGQVWHDITGNKPGTVTINADGWANFSVNGGSVS   480
4  HPNSGLATIMSDGAGGSKWMFVGRNKAGQVWSDITGNRTGTVTINADGWGNFSVNGGSVS   480

                490        500        510        520        530        540
                |          |          |          |          |          |
1  VWVKQ                                                           485
3  VWVPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAW                            514
2  IWVKR                                                           485
4  IWVNK                                                           485
```

FIG. 3